

The intron sequences between exons 2 - 3 and exons 18 - 19 are missing (introns: small letters, exons: capital letters). Small letters in the first exon indicate nucleotides that have not been unambiguously determined.

Exon 1

1 CGGGTGAATC CCGGCGCCGC GCCCCGGACC CGCAGCTCCC TGCACCTCTC
51 CCTCCCAGCC GCTTTAACAC CCACACCCCA CAGTCTCTCC CACG_sCCGCG
101 CCTTGGCGGC CCCACTGAAT CCCTACGCGG GGCCCAGCGG TACCGGGAGA
151 CCGGGCTAGC CTATGGGAGC GCCCAGATAA CGCGGGTTGG GGGCGCCCCGC
201 GCCC_cCATCC CCGCCAGCA **T** GACTCGATCG CGCCCCCTCA GAGAGCTGCC
251 CCCGAGTTAC ACACCCCCAG CTCGAACCGC AGCACCCCAG gtgagtagag
301 ggggagctgg aagaaggaag agagcggagc caggtctgtc actcgggcct
351 ctgcaagggtt tgtatgtct tgaagtgccg agtgtcatta gatgtctgaa
401 ggcaagttag agccagcacc gcaagcaagt tgtcggtgtg tgtcggtgtg
451 tctgtgccgg tgtctcctca tcgtctggcc agtgagaatg aatgtctgtg
501 gttcacctc tgtgtccacc cgacgacagg tgtgtgtaca tatgtatcct
551 gctctcagaa aatgggccta tgccgcccgg cgcggtgact cacgcctgta
601 atcccaacac tgggaggctg aggcaaggcag attacctgag gtcaggagtt
651 cgagaccagc caggccaaca tggggaaact ctgtctctac taaaaataaaa
701 aattagcagg gcgtggtggc gggcgctgt agtcccaact actcgaggagg
751 ctgagggcagg agaatctctt gaacctggga ggcggaggtt gcagtcaagc
801 cgagatcaca ccactgcact ccagccaggg caacagagcg agatgcgtct
851 caaaaaaaaaa aaaaaaaaaa aaaaggagag aaaacaaaaa gaaaagaaaag
901 gaaaataggc ctatgccttc ctcaggtgtg tgctggggat ggtgggtgtt
951 acatottcca agtctggcc tggatgtgtg ttgggtgtcc ctgtcccaca
1001 tccagaaatc aagaagcag ggctggcag cagatataca gggtgagaag

Fig. 1

2/13

1051 ggaaggattt catgcattgt tacagtgatg cctggctgac ccttctcttt
 EXON 2
 1101 ccatcccagA TCCTAGCTGG GAGCCTGAAG GCTCCACTCT GGCTTCGTGC
 1151 TTACTTCCAG GGCCCTGCTCT TCTCTCTGGG ATGCAGGGATC CAGAGACATT
 1201 GTGGCAAAGT GCTCTTTCTG GGACTGTTGG CCTTTGGGGC CCTGGCATT
 1251 GGTCTCCGCA TGGCCATTAT TGAGACAAAC TTGGAACAGC TCTGGGTAGA
 1301 AGTGGGCAGC CGGGTGAGCC AGGAGCTGCA TTACACCAAG GAGAAGCTGG
 1351 GGGAGGAGGC TGCATACACC TCTCAGATGC TGATACAGAC CGCACGCCAG
 1401 GAGGGAGAGA ACATCCTCAC ACCCGAAGCA CTTGGCTTCC ACCTCCAGGC
 1451 AGCCCTCACT GCCAGTAAAG TCCAAGTATC ACTCTATGGG AAG.....
 1501
 1551 tgagtctggc tgagccccctg agcagctggg ggcgaggcgt gctgtggggg
 1601 ttctggagtg ggaatccccct tcttctgctg atctcctatg cccctggcta
 EXON 4
 1651 ttgcagTCCT GGGATTGAA CAAAATCTGC TACAAGTCAG GAGTTCCCCCT
 1701 TATTGAAAAT GGAATGATTG AGCGGgtaaag tgcctgaga gggagtagag
 1751 gcagaacttt ttctgttagcg tgggaggact cagagaccga gcaagccccca
 1801 cagcctgcaa tctgccccct taaaactaag gagggggatt gcagagggca
 1851 tcctacaaag gttgtggggc aggactgacg tggccgggg tatccctggc
 EXON 5
 1901 agATGATTGA GAAGCTGTTT CCGTGGCGTGA TCCTCACCCCC CCTCGACTGC
 1951 TTCTGGGAGG GAGCCAAACT CCAAGGGGGC TCCGCCTACC TGCCgtgagt
 2001 gccactcctg gggccctgct tcatctccccg ctggggactc tcccagcaga
 2051 aaggaggggt ctggggatg aggatgatca aaaccttacc aaggtcctaa
 2101 ttacctccca ggcaggaac agagagcatg ggcttcccca aggctctctc
 2151 cacatcctcc ttctctttcc ctctcaagga aggaagaccc gacttattta
 2201 cacaaaacta aacacaaaaga tctgtaaagat ctgagcaaag gagaaaaaaga
 2251 tccccacaaa gaggcttgc tggggaaat tacctaggtg tttgctaaagc
 2301 cattgccag gccagaaaaga aaacctgcta caggcatgtg cctgtctggtt
 2351 gtatattaga accaaggcaca cagcttggta aggaactcag tggggccttt

Fig. 1 (cont.)

3/13

2401 ctggccctt tctatgtatt aggttaaccct gccctgatat tcgtctcaga
 2451 cccttgtaact cttctacagc tcactgttagc accctggtgg gccccatgcag
 2501 cctggcagtt ctgagaagct gaggcttgca caccctccat atggaaggac
 2551 aaatcggcag ataagaggag ggtggggtagc agcatggcgc cccagcagca
 2601 gtttggagcc tgggttttcg tccctgaccc tcaccaacta taggctttc
 EXON 6
 2651 cctcagCGGC CGCCCGGATA TCCAGTGGAC CAACCTGGAT CCAGAGCAGC
 2701 TGCTGGAGGA GCTGGGTCCC TTTGCCTCCC TTGAGGGCTT CCGGGAGCTG
 2751 CTAGACAAGG CACAGGTGGG CCAGGCCTAC GTGGGGCGGC CCTGTCTGCA
 2801 CCCTGATGAC CTCCACTGCC CACCTAGTGC CCCCCAACCAT CACAGCAGGC
 2851 AGgtgggttc caaccaggtc tgccaggaa aggctgtttt cttcccttt
 2901 cccttcctca tactcctgtg ttctggggaa gctgactgct ctgtgcctg
 2951 accccccact tcctggccat tattaccctg ctcccacagt gccaggcccc
 3001 caatgttcca ttcccattca gttatcctac ggagccctca agtggtatat
 3051 atgaatccct tttccctttt ctaagcctag ataaggctgg acttctttt
 3101 tttttttttt ttgagtctca ctctgtcacc caggctggag tgcagtagtt
 3151 cgatcttggc tcactgcaac ctggctcaa gcaattctcc tgccttagcc
 3201 tcctgagtag ctgggattac aggtgcccac caccatgccc ggctaatttt
 3251 tattagcctc ccaaagtgct gggattacag gcgtgagcca ctgcgcctgg
 3301 ccaaggctgg acttttatac aaaatagact aatacaggga aactaagaac
 3351 acagcaggtta agcatgaata tcatacctgg tttcccaggt ttctttgtgg
 3401 ccctgcaaatt gtggtaactt tttcagaatc cggcagttac accagctcct
 3451 cccagaagcc tacttccagg ctctgtctc ccctggggc ttctgtctg
 3501 cgggatacta gctgttcaact cctgcagagc agtcaagagg ctcagaataag
 3551 ttacctacac tccagcccta ctgagcttca tggcagcgtg gttcctggag
 3601 gtggaaagccc agggacactc agttatccac ggccagggcc ttgagcatta
 EXON 7
 3651 acccctcctg ttccccctcca gGGCTCCCAA TGTGGCTCAC GAGCTGAGTG
 3701 GGGGCTGCCA TGGCTTCTCC CACAAATTCA TGCACTGGCA GGAGGAATTG

Fig. 1 (cont.)

WO 00/20037

PCT/SE99/01784

4/13

Fig. 1 (cont.)

5/13

5101 CGGGCACCAAG TGTCGTACTC ACATCCATCA ACAACATGGC CGCCTTCCTC
 5151 ATGGCTGCCCGTCCAT CCCTGGCGCTG CGAGCCTTCT CCCTACAGGC
 5201 GGCCATAGTG GTTGGCTGCA CCTTTGTAGC CGTGATGCTT GTCTTCCCAG
 5251 CCATCCTCAG CCTGGACCTA CGGCAGGCAGC ACTGCCAGCG CCTTGATGTG
 5301 CTCTGCTGCT TCTCCAGgt a ctgcgtgaga cccagccct tcctcccgta
 5351 acccacgcca gcctgtcccc tcaccagcat ttcaaggcac, agacctgtca
 EXON 13
 5401 tccactctct acctcttcca gTCCCTGCTC TGCTCAGGTG ATTCAAGATCC
 5451 TGCCCCAGGA GCTGGGGGAC GGGACAGTAC CAGTGGGCAT TGCCCACCTC
 5501 ACTGCCACAG TTCAAGCCTT TACCCACTGT GAAGCCAGCA GCCAGCATGT
 5551 GGTCAACCATC CTGCCTCCCC AAGCCCACCT GGTGCCCTCA CCTTCTGACC
 5601 CACTGGGCTC TGAGCTCTTC AGCCCTGGAG GGTCCACACG GGACCTTCTA
 5651 GGCCAGGAGG AGGAGACAAG GCAGAAGGCA GCCTGCAAGT CCCTGCCCTG
 5701 TGCCCCGCTGG AATCTTGCCC ATTTCGCCCC CTATCAGTTT GCCCCGTTGC
 5751 TGCTCCAGTC ACATGCTAAG gtaagactgg qcagagcagg gcagagactt
 5801 agcatctctg ggcccagaag ggcagagagg gcttagtcca ctgcctgagg
 EX
 5851 ggctgggggc agccctgggg tctccagctt agttgctaca tcccgcaagGC
 XON 14
 5901 CATCGTGCTG GTGCTCTTG GTGCTCTTCT GGGCCTGAGC CTCTACGGAG
 5951 CCACCTTGGT GCAAGACGGC CTGGCCCTGA CGGATGTGGT GCCTCGGGGC
 6001 ACCAAGGAGC ATGCCCTCCT GAGGCCAG CTCAGGTACT TCTCCCTGTA
 6051 CGAGGTGGCC CTGGTGACCC AGGGTGGCTT TGACTACGCC CACTCCAAC
 6101 GCGCCCTCTT TGATCTGCAC CAGCGCTTCA GTTCCCTCAA GGCGGTGCTG
 6151 CCCCCACCGG CCACCCAGGC ACCCCGCACC TGGCTGCAGT ATTACCGCAA
 6201 CTGGCTACAG Ggtgagaggc gaggagacgg gcagggaggg gtgctgcagg
 6251 gagaaaacgcc ctggggccac cagctaatacg aaccctatcc tggctccccc
 EXON 15
 6301 cagGAATCCA GGCTGCCTT GACCAGGACT GGGCTTCTGG GCGCATCACC
 6351 CGCCACTCGA CCGCAATGGC TCTGAGGATG GGGCCCTGGC CTACAAGCTG
 6401 CTCATCCAGA CTGGAGACGC CCAGGAGCTT CTGGATTCA GCCAGgttgg

Fig. 1 (cont.)

6/13

6451 gagagggctg gaggggtcca ctagtacagg ggctgcaggc ctcctgggcc
 EXON 16
 6501 caggccttca gcctctctcg cctctgcagC TGACCACAAG GAAGCTGGTG
 6551 GACAGAGAGG GACTGATTCC ACCCGAGCTC TTCTACATGG GGCTGACCGT
 6601 GTGGGTGAGC AGTGACCCCC TGGGTCTGGC AGCCTCACAG GCCAACTTCT
 6651 ACCCCCCACC TCCTGAATGG CTGCACGACA AATACGACAC CACGGGGAG
 6701 AACTTCGCA gtgagtcctg gggggagctc ggcaagagcc tcagcctcgc
 6751 ccacacaaggc cctgagcctg aggccctgcc cactctgccc cgtgctcacc
 EXON 17
 6801 gcctgtccc tctccctctt ctcccttccc ctccctcca cagTCCCGCC
 6851 AGCTCAGCCC TTGGAGTTTG CCCAGTTCCC TTTCTGCTG CGTGGCCTCC
 6901 AGAAGACTGC AGACTTTGTG GAGGCCATCG AGGGGGGCCCG GGCAGCATGC
 6951 GCAGAGGCCG GCCAGGCTGG GGTGCACGCC TACCCCAAGCG GCTCCCCCTT
 7001 CCTCTTCTGG GAACAGTATC TGGGCTGCG GCGCTGCTTC CTGCTGGCCG
 7051 TCTGCATCCT GCTGGTGTGC ACTTTCTCG TCTGTGCTCT GCTGCTCCTC
 7101 AACCCCTGGA CGGCTGGCCT CATAgtgagt gcttgcagga gtggggacag
 7151 agacacccca cccttccctg cccagcctgt cattccctccct gecaggagcc
 EXON 18
 7201 ctctgtgago cctgtctccc tcagGTGCTG GTCCTGGCGA TGATGACAGT
 7251 GGAACTCTTT GGTATCATGG GTTCTCTGGG CATCAAGCTG AGTGCATCC
 7301 CCGTGGTGAT CCTTGTGGCC TCTGTAGGCA TTGGCGTTGA GTTCACAGTC
 7351 CACGTGGCTC TGGGCTTCCT GACCACCCAG GGCAGCCGGA ACCTGCAGGC
 7401 CGCCCATGCC CTTGAGCACA CATTGCCCT CGTGACCGAT GGGGCCATCT
 7451 CCACATTGCT GGGTCTGCTC ATGCTTGCTG GTTCCCACCT TGACTTCATT
 7501 GTAAG.....
 7551 gtagggaggg ctcggggcag ggaggcaggg ctcaggacag
 EXON 20
 7601 gcctgggctg actcccccca caccctaccc ctagGTACTT CTTTGCAGGC
 7651 CTGACAGTGC TCACGCTCCT GGGCCTCCTC CATGGACTCG TGCTGCTGCC
 7701 TGTGCTGCTG TCCATCCTGG GCCCCCGGCC AGAGgtgacc acaccctcgg
 7751 caccatccct ctactccctg cccaaaggac ggggttagggg gaggcaagg

Fig. 1 (cont.)

7/13

7801 aaggacaga gccctgtggc ccacagacag gtacctcccc aacaggtgcc
7851 accagctgaa ggtggcagcc tcctccttcc cccagacacc atgttcctgc
7901 ccctcagccc tcctggcttc ttcatggac ccaccttaga cttttaggat
7951 ccagaacaag gtgcagggtt tgccccaggc ctcaacatcc tgtgcctgc
8001 cagctctcat atcctgctgg agaccaacaa gggccccagc ttcccaacag
8051 tcatggtaat ccccagcgag atgctaaagg ggacgggagc cccagggggcc
EXON 21
8101 cgtgggctta ctggggctgg tgtctccca cagGTGATAC AGATGTACAA
8151 GGAAAGCCA GAGATCCTGA GTCCACCCAGC TCCACAGGGA GGCGGGCTTA
8201 Ggtggggggc atcctcctcc ctgccccaga gcttgccag agtgaactacc
8251 tccatgaccg tggccatcca cccacccccc ctgcctggcgtg cctacatcca
8301 tccagccct gatgagcccc cttggtcccc tgctgtcact agctctggca
8351 acctcagttc caggggacca ggtccagcca ctgggtgaaa gagcagctga
8401 agcacagaga ccatgtgtgg ggcgtgtgg gtcactggga agcactgggt
8451 ctgggtgttag acgcaggatg gacccttggg gggctctgt gctgctgcatt
8501 cccctctccc gacccagctg tcattggcct ccctgatatac catacagaac
8551 agccacccgat ttgcacatcc aggcctgtgt gagectgtat ctgtgtcact
8601 tgagagtgaa agctggcaact tggggctgca gtgcagccct gtcccccttc
8651 ccacccaca ccactgcctg cccagctgac caagcctgag ggaccctcca
8701 gcacccctcc gtctggtgac tcctggcag gtcctccata tcctgcccc
8751 cctcctacca catccattat ttatatgaaa atgtctatcc ttgttagtata
8801 catacatgtt agctatgtat aaagtttat ttttaaaga atgaaatata
8851 ttctatgtga agctatgtat aaagtttat ttttaaaga atgaaatata
8901 ttctatgtga actaatctcg aaagtttat ttttaaaga atgaaatata
8951 ttctatgtgt gcaagtgaac attagcttca gttgttttt tttggacaga
9001 gtggggagtt tgcaagtgaa cattagctat tggaaggagc ttctctggtg
9051 ccaggacctg aggtattage ttctctagtt ctgggtggaa aagacccca
9101 attctggatt ttgtcatat acttgtaac atcatcttggg ttaagtgcct

Fig. 1 (cont.)

8/13

9151 actatacacaa acgataacaa attttgttgg ttgtaaaatcc tactgggttc
9201 aatctggaga ccgagagcag aaaaaaaaaga accccactgt gtggcttca
9251 gagccaccat attccagcct gcccgtctct ccagactcac ctccacacctac
9301 ctgcttcacc cgacacggaa acggcaaggc agaggggcaa agccatgcag
9351 caggtggaag gcgaggtgga ggcagatcag gaaagcagcc agttgaagca
9401 gagagaggtc aacagggtct ggggagcttc tcaggaggtt tttggaccca
9451 gggaaaggag ccaggttcca gagcaacctc caaggcaaag gcctctgtaa
9501 gttggttgtc ctgacagccg agaggtgtct ttggccatgc agccagtgg
9551 tcagttgcgg gaactgctca gaaactgagg tgcttagcagt tagtgaggac
9601 acagcgtaag ttgtttgttc tttgtaaaatggtaa gaaacagctcc actaaggcaga
9651 ggccttgaag agtggccaca gcccgttggaaat agagcacaaaaa gcccacccaa
9701 gagggcggtggg gaggtttgca actgcccctt cccagccata gcttaggacc
9751 catagtcttag ttcacataga ccctgggttc caaccaccca ctcaccaggaa
9801 atgatcccac cccaggaaca atgcgttctc acatcccacc ccacctggac
9851 aaaggccagg aaatcatgtt ctgacaaaaa gatacaacaa caaaaacaac
9901 aacaacaaaa aacgcctatt gcaattgaat ccacgctaaa atgcctaaaa
9951 agctcaagag aagcggttag ttggcagaga accttagagta gggggtgcaa
10001 ccagcaggcc caagggaggg aggctgcatt tgggtccagc agtgtttggg
10051 tcaccaagaa gggccttcta ggtggagcag agagagctca ccaggccaga
10101 atagtgcaaa gggggtcagc cctcagtgcc acttaccagc ggagtaaccc
10151 tgggcaagtt agccagcctc actaagcctc cccatcttca tctttccagG
XON 22
10201 CCCGAGGAGA TC**TAG**CCTCT GCCTCCCACC CCAGCACCCC CTCATCAGAC
10251 ACAAGGAGCG CCACTGTCTG GACAGGCTGA ATTGGTCTTC GGGTCCCTAA
10301 TTTCTCATAC GCCATTCCCT CTGCCTAGAA CACTTTCTCA CCTCCCTTG
10351 ATGTGACCCCC ATATCACCCCT TCGAGGTGAA TTGGATCGGA TGCCATCTCC
10401 TCCAGGAGGG GTGGGGTCGT GCCTCCTGTG AGGTCCAGT GCCCCTGAGT
10451 GTCTGTGCC CCGTCTTCC CCGTCCCTCT CTCTAAGCCCC GGAGGCTTAC

Fig. 1 (cont.)

9/13

10501 TGCAGGTAAG GACGGCGGGA CAGGACCTTA ACCGCTGGGA CGAACACCCAG
10551 CTCCGAAAG GACTCCGCAC CCGGCGCCGC CCACGGGGTG CGGGTCCCAG
10601 GAGGACCAAGC AGAGAGGAGC ATAGGAGAGC AAAGGAGATC AGTGACCCAT
10651 GGCTTCCCCG GTGGCGCGGA ACAGCCCGGA GCCGCCTGTG ATTTGCATAC
10701 CCATGGTGCA CCACGAAAAG ATACCCCTCAA GATGCTTGCA CTCCCTCTGT
10751 GCGCGCATTT CTGCACTGTT TTAGAGCATG ATGCCTCTTA CACGCATCTG
10801 TGTGCATAAA CTACATATAG GGAGTGGCGTA CCACGCAGGC ATCCAACAAAC
10851 CATAAGTGTG TTAAGTGTGA GTTCTCCCTG CGAGGTTCGA AGCGGAAGTC
10901 ACGAATATAC TCGGGTTTCT CTTCAAAGCG CATAAAATCTT TCGCCTTTTA
10951 CTAAAGATTT CCGTGGAGAG AAAGTTGTGA GTTTTTATTC AATTTTTTG
11001 GGCTCTTAT TTCTGAGGC TACATTTTA AGTATTAAAAA GTTAGGCAAC
11051 TACAAAAAAA AAAAAAAA

Fig. 1 (cont.)

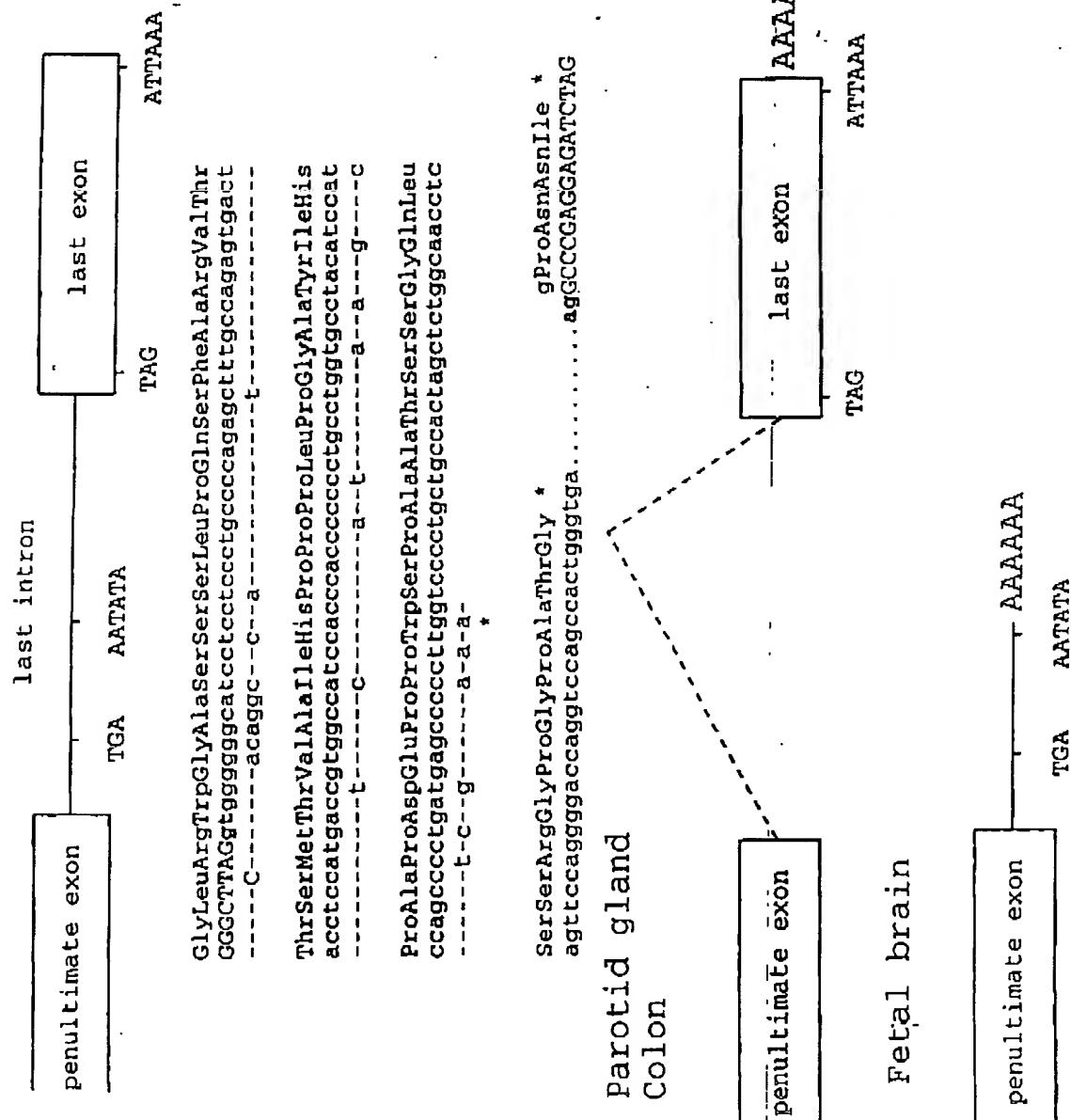
10/13

1MTRSPPLRELP..... 11
 1 MASAGNAAEQDQDRGGGGSGCIGAPGRPAGGGRRRTGGLRRAAPDRDYL 50
 12 ..PSYTPPPARTAAPQI...LAGSLKAPLWLRAYFQGGLFSLGGGIQRHCG 56
 51 HRPSCDAA.FALEQISKGKATGRKAPLWLRAKFQRLLFKLGGYIQKNCG 99
 57 KVLFGLLAFGALALGLRMAIETNLEQLWVEVGSRVSQELHYTKEKLGE 106
 100 KFLVVGLLIFGAFAVGLKAANLETNVEELWVEVGGRVSRELYTRQKIGE 149
 107 EAAYTSQMLIQTARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDL 156
 150 EAMFNPOLMCIQTPKEEGANVLTTEALLQHEDSALQASRVHVYMYNROWKL 199
 157 NKICYKSGVPLIENGMIERMIEKLFPCVILTPLCDFWEGAKLQGGSAYLP 206
 200 EHLCYKSGELITEGYMDQIEYLYPCLIITPLDCFWEAKLQSGTAYLL 249
 207 GRPDIQWTNLDPEQLLEELGPFA.SLEGFRELLDKAQVGQAYVGRPCLHP 255
 250 GKPPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGYMDRPCLNP 299
 256 DDLHCPPSAPNHHSRQAPNVAHELGGCHGFSHKFMHWQEELLGGMARD 305
 300 ADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKN 349
 306 PQGELLRAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAW 355
 350 STGKLVSAAHALQTMFQLMTPKQMYEHFKGYEYVSHIINWNEDKAAILEAW 399
 356 QRRFVQLAQEALPENASQQIHAFSSTLDDILHAFSEVSAARVVGGYLLM 405
 400 QRTYVEVVHQSVAQNSTQKVLSTTTLDDILKSFSDVSVIKVASGYLLM 449
 406 LAYACVTLRWDCQAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAAT 455
 450 LAYACLTMLRWDCSKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAAT 499
 456 TQVLPFLALGIGVDDVFLLAHAFTEALPG..TPLOERMGECLQRTGTSVV 503
 500 TQVLPFLALGVGVDDVFLLAHAFSETGQNKRIPFEDRTGECLKRTGASVA 549
 504 LTSINNMMAFLMAALVPIPALRAFLQAAIVVGCTFVAVMLVFPAILSLD 553
 550 LTSISNVTAFFMAALIPIPALRAFLQAAVVVFNFAMVLLIFPAILSMQ 599
 554 LRRRHQCQLDVLCFFSSPCSAQVIQILPQELGDGT.....VPVG 592
 600 LYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSH 649
 593 IAH.....LTATVQAFTHCEASSQHVVTILPPQAH.....VPPPSDPLGS 633
 650 FAHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSC 699

Fig. 2A

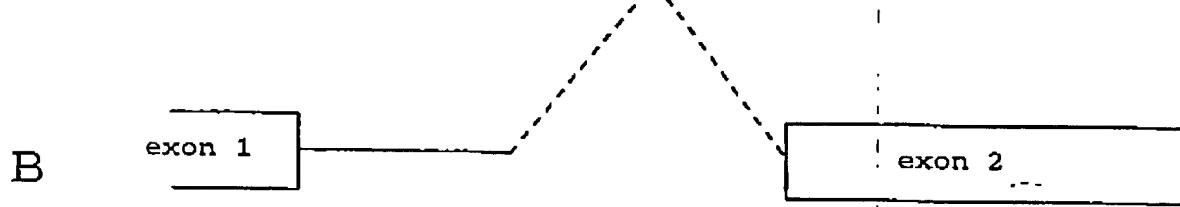
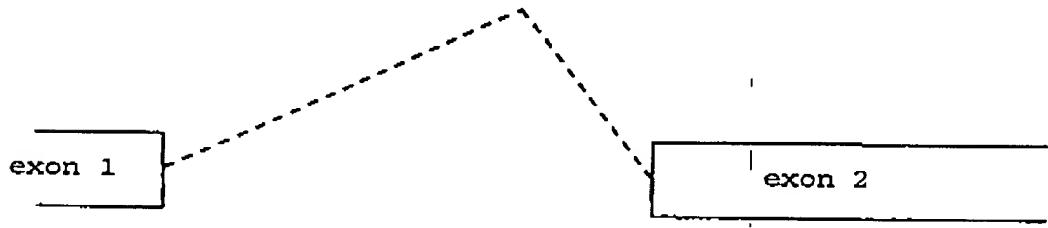
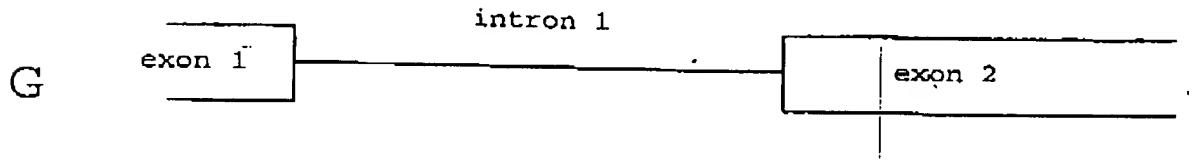
11/13

Fig. 2B Genomic



12/13

Fig. 2C



09/807007

WO 00/20037

PCT/SE99/01784

13/13

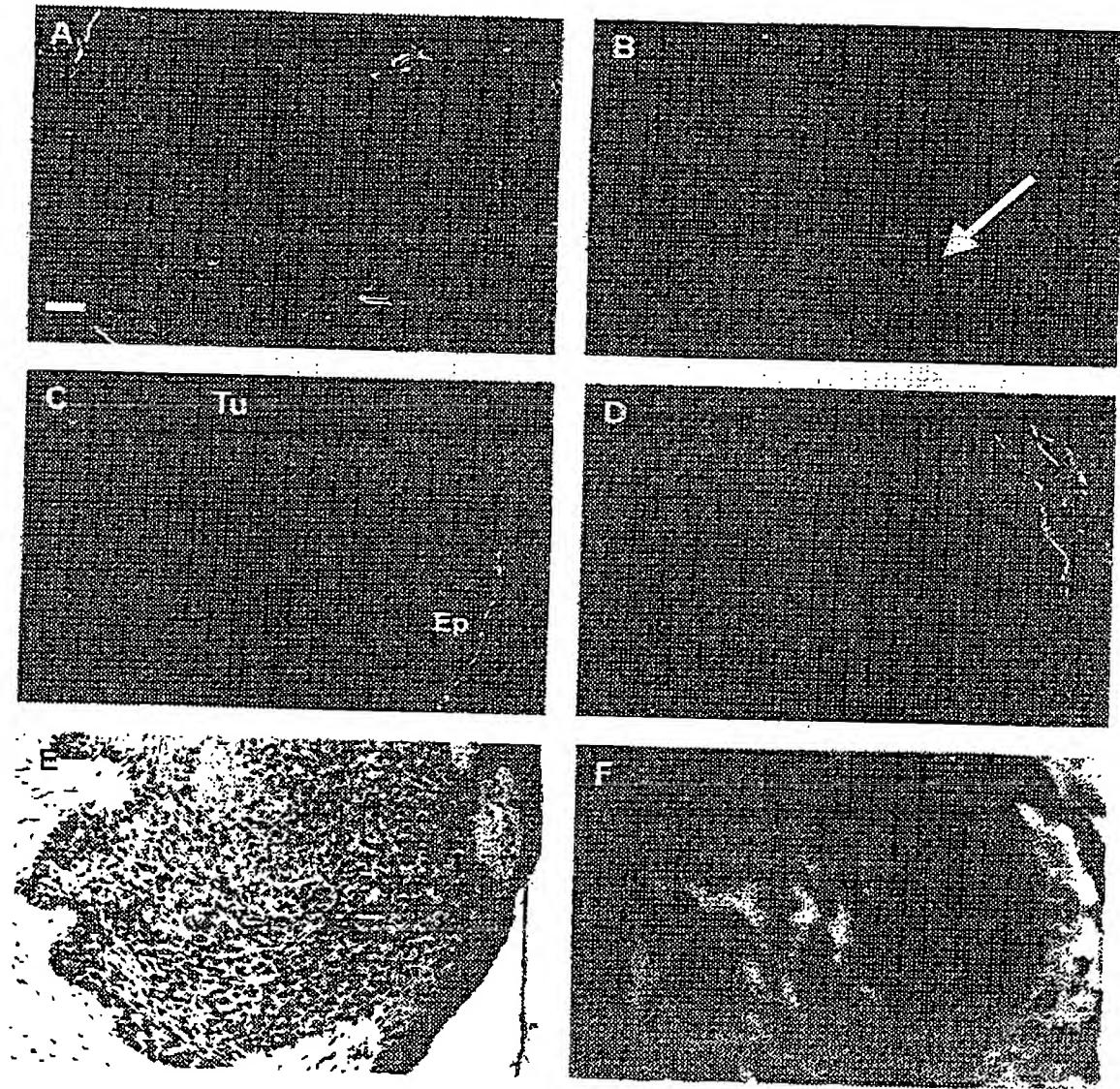


Fig. 3